

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Adams, Camilia W.
 Ashkenazi, Avi J.
 Chuntharapai, Anan
 Kim, Kyung J.

10 (ii) TITLE OF INVENTION: Apo-2 Receptor

(iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Genentech, Inc.
 (B) STREET: 1 DNA Way
 (C) CITY: South San Francisco
 (D) STATE: California
 (E) COUNTRY: USA
 20 (F) ZIP: 94080

(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 25 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
 30 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
 35 (A) NAME: Marschang, Diane L.
 (B) REGISTRATION NUMBER: 35,600
 (C) REFERENCE/DOCKET NUMBER: P1101R2

(ix) TELECOMMUNICATION INFORMATION:
 40 (A) TELEPHONE: 650/225-5416
 (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 411 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
 1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
 20 25 30

55 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
 35 40 45

60 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
 50 55 60

	Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	
					65					70					75	
5	Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	
					80					85					90	
	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	
					95					100					105	
10	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	
					110					115					120	
	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	
					125					130					135	
15	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro	
					140					145					150	
	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
20					155					160					165	
	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	
					170					175					180	
25	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	
					185					190					195	
	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
					200					205					210	
30	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	
					215					220					225	
	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	
35					230					235					240	
	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	
					245					250					255	
40	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	
					260					265					270	
	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	
					275					280					285	
45	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	
					290					295					300	
	Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp	
50					305					310					315	
	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg	
					320					325					330	
55	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu	
					335					340					345	
	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp	
60					350					355					360	

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
 365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
 5 380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

Ala Asp Ser Ala Xaa Ser
 410 411

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1799 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50
 GCGCCCAACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100
 CCACGGGCGCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
 Met Glu
 1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
 5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
 20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
 Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
 30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
 Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
 45 50

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
 Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
 55 60 65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
 85 90

	TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	457
	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	
	95						100					105		
5	TGG	AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC	AGG	TGT	496
	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	
				110				115						
10	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCC	TGC	ACC	ACG	ACC	535
	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	
	120					125					130			
15	AGA	AAC	ACA	GTG	TGT	CAG	TGC	GAA	GAA	GGC	ACC	TTC	CGG	574
	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	
			135				140						145	
20	GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	613
	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	
					150				155					
25	CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGC	691
	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
				175				180						
30	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
	185					190					195			
35	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
			200				205						210	
40	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
					215				220					
45	GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	886
	Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
				240				245						
50	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	925
	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
	250					255					260			
55	CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	964
	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
			265				270						275	
60	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA	GCT	1003
	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	
					280				285					

GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
 290 295 300

5 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
 305 310

10 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
 315 320 325

15 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340

20 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 345 350

TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365

25 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375

30 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390

35 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
 Ala Asp Ser Ala Xaa Ser
 410 411

40 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

45 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTTACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

50 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

55 GCGCGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 70 base pairs
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50
GCTAAAGCTG AGGCAGCGGG 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
30 35

	GCC	GAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGT	GTG	GAA	153
	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Glu	
		40					45					50		
5	CGG	CCG	GGG	GGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	192
	Arg	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
			55						60					
10	GGA	TTC	ACC	TTT	GAT	GAT	TAT	GGC	ATG	AGC	TGG	GTC	CGC	231
	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly	Met	Ser	Trp	Val	Arg	
		65				70					75			
15	CAA	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCT	GGT	ATT	270
	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile	
			80					85					90	
20	AAT	TGG	AAT	GGT	GGT	AGC	ACA	GGA	TAT	GCA	GAC	TCT	GTG	309
	Asn	Trp	Asn	Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	
				95						100				
25	AAG	GGC	CGA	GTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	348
	Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
		105					110					115		
30	TCC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	387
	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				120					125					
35	ACG	GCC	GTA	TAT	TAC	TGT	GCG	AAA	ATC	CTG	GGT	GCC	GGA	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Ile	Leu	Gly	Ala	Gly	
		130				135					140			
40	CGG	GGC	TGG	TAC	TTC	GAT	CTC	TGG	GGG	AAG	GGG	ACC	ACG	465
	Arg	Gly	Trp	Tyr	Phe	Asp	Leu	Trp	Gly	Lys	Gly	Thr	Thr	
			145					150					155	
45	GTC	ACC	GTC	TCG	AGT	GGT	GGA	GGC	GGT	TCA	GGC	GGA	GGT	504
	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
				160						165				
50	GGC	AGC	GGC	GGT	GGC	GGA	TCG	TCT	GAG	CTG	ACT	CAG	GAC	543
	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	Thr	Gln	Asp	
		170					175					180		
55	CCT	GCT	GTG	TCT	GTG	GCC	TTG	GGA	CAG	ACA	GTC	AGG	ATC	582
	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val	Arg	Ile	
				185					190					
60	ACA	TGC	CAA	GGA	GAC	AGC	CTC	AGA	AGC	TAT	TAT	GCA	AGC	621
	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	
		195				200					205			
65	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	GCC	CCT	GTA	CTT	GTC	660
	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	
			210					215					220	
70	ATC	TAT	GGT	AAA	AAC	AAC	CGG	CCC	TCA	GGG	ATC	CCA	GAC	699
	Ile	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	
					225					230				

CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738
 Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu
 235 240 245

5 ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777
 Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr
 250 255

10 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
 260 265 270

15 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 275 280 285

20 GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894
 Ala His His His His His His Gly Ala Ala Glu Gln Lys
 290 295

CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 300 305 309

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 939 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153
 Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 40 45 50

CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231
 Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg
 65 70 75

	CAG	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTG	GCC	AAC	ATA	270
	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile	
			80					85					90	
5	AAG	CAA	GAT	GGA	AGT	GAG	AAA	TAC	TAT	GTG	GAC	TCT	GTG	309
	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	
				95						100				
10	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	348
	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
		105					110					115		
15	TCA	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	387
	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
				120					125					
20	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	CTT	TTA	AAG	GTC	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Leu	Leu	Lys	Val	
	130					135					140			
25	AAG	GGC	AGC	TCG	TCT	GGG	TGG	TTC	GAC	CCC	TGG	GGG	AGA	465
	Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe	Asp	Pro	Trp	Gly	Arg	
			145				150						155	
30	GGG	ACC	ACG	GTC	ACC	GTC	TCG	AGT	GGT	GGA	GGC	GGT	TCA	504
	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	
				160						165				
35	GGC	GGA	GGT	GGT	AGC	GGC	GGT	GGC	GGA	TCG	TCT	GAG	CTG	543
	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	
		170				175						180		
40	ACT	CAG	GAC	CCT	GCT	GTG	TCT	GTG	GCC	TTG	GGA	CAG	ACA	582
	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	
			185						190					
45	GTC	AGG	ATC	ACA	TGC	CAA	GGA	GAC	AGC	CTC	AGA	AGC	TAT	621
	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	
	195				200					205				
50	TAT	GCA	AGC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	GCC	CCT	660
	Tyr	Ala	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	
			210					215					220	
55	GTA	CTT	GTC	ATC	TAT	GGT	AAA	AAC	AAC	CGG	CCC	TCA	GGG	699
	Val	Leu	Val	Ile	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	
				225					230					
60	ATC	CCA	GAC	CGA	TTC	TCT	GGC	TCC	AGC	TCA	GGA	AAC	ACA	738
	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Thr	
		235					240					245		
65	GCT	TCC	TTG	ACC	ATC	ACT	GGG	GCT	CAG	GCG	GAA	GAT	GAG	777
	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	Glu	
				250				255						
70	GCT	GAC	TAT	TAC	TGT	AAC	TCC	CGG	GAC	AGC	AGT	GGT	AAC	816
	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	
	260				265						270			

CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855
 His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 275 280 285

5 GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894
 Gly Ala Ala Ala His His His His His His Gly Ala Ala
 290 295

10 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
 300 305 310

GCA TAG 939
 Ala
 15 312

(2) INFORMATION FOR SEQ ID NO:8:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 933 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 1 5 10

35 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 15 20 25

40 CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

45 GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val
 40 45 50

50 CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

55 GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg
 65 70 75

CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
 80 85 90

TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
 95 100

	AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	348
	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	
		105					110					115		
5	ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC	387
	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
			120						125					
10	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	AGG	GGC	TAC	TAC	426
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	
		130				135					140			
15	TAC	ATG	GAC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC	465
	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	
			145				150						155	
20	TCC	TCA	GGT	GGA	GGC	GGT	TCA	GGC	GGA	GGT	GGC	TCT	GGC	504
	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
				160					165					
25	GGT	GGC	GGA	TCG	CAG	TCT	GTG	TTG	ACG	CAG	CCG	CCC	TCA	543
	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	
		170				175					180			
30	GTG	TCT	GGG	GCC	CCA	GGA	CAG	AGG	GTC	ACC	ATC	TCC	TGC	582
	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	
			185				190							
35	ACT	GGG	AGA	AGC	TCC	AAC	ATC	GGG	GCA	GGT	CAT	GAT	GTA	621
	Thr	Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	
		195				200					205			
40	CAC	TGG	TAC	CAG	CAA	CTT	CCA	GGA	ACA	GCC	CCC	AAA	CTC	660
	His	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	
			210				215						220	
45	CTC	ATC	TAT	GAT	GAC	AGC	AAT	CGG	CCC	TCA	GGG	GTC	CCT	699
	Leu	Ile	Tyr	Asp	Asp	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	
				225					230					
50	GAC	CGA	TTC	TCT	GGC	TCC	AGG	TCT	GGC	ACC	TCA	GCC	TCC	738
	Asp	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Thr	Ser	Ala	Ser	
		235				240					245			
55	CTG	GCC	ATC	ACT	GGG	CTC	CAG	GCT	GAA	GAT	GAG	GCT	GAT	777
	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	
			250				255							
60	TAT	TAC	TGC	CAG	TCC	TAT	GAC	AGC	AGC	CTG	AGG	GGT	TCG	816
	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser	Leu	Arg	Gly	Ser	
		260				265				270				
65	GTA	TTC	GGC	GGA	GGG	ACC	AAG	GTC	ACT	GTC	CTA	GGT	GCG	855
	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Ala	
			275				280						285	
70	GCC	GCA	CAT	CAT	CAT	CAC	CAT	CAC	GGG	GCC	GCA	GAA	CAA	894
	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	
				290					295					

AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 300 305 310

5 TAG 933

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 309 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 1 5 10 15
 20 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
 20 20 25 30
 Phe Tyr Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln
 35 40 45
 25 Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser
 50 55 60
 Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp
 65 70 75
 30 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
 80 85 90
 Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
 95 100 105
 Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 110 115 120
 40 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 125 130 135
 Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp
 140 145 150
 45 Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 155 160 165
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln
 170 175 180
 50 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr
 185 190 195
 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln
 200 205 210
 Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn
 215 220 225
 60

	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	230	235	240
5	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	245	250	255
	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His	260	265	270
10	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ala	Ala	275	280	285
	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile	290	295	300
15	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala							305	309	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

	Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile	1	5	10	15
30	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	20	25	30	
	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gly	Val	Gln	Leu	Val	Glu	35	40	45	
	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	50	55	60	
40	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Trp	Met	Ser	Trp	65	70	75	
	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile	80	85	90	
45	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly	95	100	105	
	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	110	115	120	
	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	125	130	135	
55	Ala	Arg	Asp	Leu	Leu	Lys	Val	Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe	140	145	150	
	Asp	Pro	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	155	160	165	

	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu
					170					175					180
5	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val
					185					190					195
	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser
					200					205					210
10	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
					215					220					225
	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
					230					235					240
15	Ser	Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln
					245					250					255
20	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser
					260					265					270
	Gly	Asn	His	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu
					275					280					285
25	Gly	Ala	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln
					290					295					300
	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala			
					305					310		312			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40	Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile
	1				5					10					15
	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro
					20					25					30
45	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	Gln
					35					40					45
50	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser
					50					55					60
	Cys	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp
					65					70					75
55	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile
					80					85					90
	Phe	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
60					95					100					105

	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	
					110					115					120	
5	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					125					130					135	
	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	
					140					145					150	
10	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
					155					160					165	
	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro		
					170					175					180	
15	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Thr	
					185					190					195	
	Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	His	Trp	Tyr	
20					200					205					210	
	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Asp	
					215					220					225	
25	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg	
					230					235					240	
	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu	
					245					250					255	
30	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser	Leu	Arg	
					260					265					270	
	Gly	Ser	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu	Gly	Ala	
35					275					280					285	
	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	
					290					295					300	
40	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala						
					305					310						

(2) INFORMATION FOR SEQ ID NO:12:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCGGATAAC AATTTACAC AGG 23

55

(2) INFORMATION FOR SEQ ID NO:13:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGACGGTAG T 21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg	Gly	Lys	Asp	Leu
1				5				10		12	